

SEQUENCE LISTING

<110> KEITH, TIM
 LITTLE, RANDALL D.
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 DUPUIS, JOSEE
 DEL MASTRO, RICHARD L.
 SIMON, JASON
 ALLEN, KRISTINA
 PANDIT, SUNIL

<120> NOVEL HUMAN GENES RELATING TO RESPIRATORY DISEASES AND OBESITY

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<150> 60/211,749

<151> 2000-06-14

<150> 60/146,336

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cag	gaa	ggg	acc	cgg	gtc	cac	gaa	ctg	ccc	acg	ccc	tct	cca	gga	ggg	479
Gln	Glu	Gly	Thr	Arg	Val	His	Glu	Leu	Pro	Thr	Pro	Ser	Pro	Gly	Gly	
	145					150					155					
gac	ccg	ggt	cca	cga	gct	gcc	cac	gtc	gtc	aac	ggg	aag	gga	ccc	ggg	527
Asp	Pro	Gly	Pro	Arg	Ala	Ala	His	Val	Val	Asn	Gly	Lys	Gly	Pro	Gly	
160					165					170					175	
tcc	acg	agc	tgc	cca	cgt	cct	ctc	cag	gaa	ggg	acc	cgg	gtc	cac	gaa	575
Ser	Thr	Ser	Cys	Pro	Arg	Pro	Leu	Gln	Glu	Gly	Thr	Arg	Val	His	Glu	
				180					185					190		
ctg	ccc	acg	cgc	tct	cca	gga	ggg	gac	acc	ggg	ttc	acg	agc	tgc	cca	623
Leu	Pro	Thr	Arg	Ser	Pro	Gly	Gly	Asp	Thr	Gly	Phe	Thr	Ser	Cys	Pro	
			195					200					205			
cgc	cct	ctc	cag	gaa	ggg	acc	ccg	ggt	tca	cga	gct	gcc	cac	gtc	ctc	671
Arg	Pro	Leu	Gln	Glu	Gly	Thr	Pro	Gly	Ser	Arg	Ala	Ala	His	Val	Leu	
		210					215					220				
tcc	agg	agg	gga	cac	cgg	gtt	cac	gag	ctg	ccc	acg	tcc	tct	cca	gga	719
Ser	Arg	Arg	Gly	His	Arg	Val	His	Glu	Leu	Pro	Thr	Ser	Ser	Pro	Gly	
	225					230					235					
ggg	gac	acc	ggg	ttc	acg	agc	tgc	cca	cgc	cct	ctc	cag	gag	ggg	aca	767
Gly	Asp	Thr	Gly	Phe	Thr	Ser	Cys	Pro	Arg	Pro	Leu	Gln	Glu	Gly	Thr	
240					245					250					255	

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Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser	
260 265 270	
acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct	863
Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala	
275 280 285	
gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg	911
Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg	
290 295 300	
ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc	959
Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala	
305 310 315	
ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc	1007
Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala	
320 325 330 335	
gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg	1055
Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg	
340 345 350	
cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg	1103
Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu	
355 360 365	
gac ctg ccc cca tgg acc tgg gaa cct ccc ggc tct tcc cac tcg gga	1151
Asp Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly	
370 375 380	
aag gaa ggc tct ggg cat gga ggt cgg cca ggc ccc atc ccc gta ccc	1199
Lys Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro	
385 390 395	
tgg ccc ttc ttc ctg ctt cct gtt tgt cac tgc ccc ggg gcc ttt gca	1247
Trp Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala	
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cct gca ttc cct ctc tct aga cag ggt ttc tcc tca ttg gcc agg ctg	1295
Pro Ala Phe Pro Leu Ser Arg Gln Gly Phe Ser Ser Leu Ala Arg Leu	
420 425 430	
gtc tcg aac tcc tgacctcaga cgatccacct gcctcagcct cccgaagtgt	1347
Val Ser Asn Ser	
435	
tgggattaca ggcacgagcc actgtgcccc gccatcattc ctttttactg ctgactaata	1407
gtctgctgtg tgaatccacc gctagaaacc cactcatcag ttgatgggtca tgtgggttgc	1467
ttctgctatt cgcttattat gaacagtgt ggaataaacg ttctgtgca ctcttgggca	1527
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 <213> Homo sapiens

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 35 40 45
 Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
 50 55 60
 Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
 65 70 75 80
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
 85 90 95
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 100 105 110
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
 115 120 125
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
 130 135 140
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
 145 150 155 160
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
 165 170 175
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
 180 185 190
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270

Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
 355 360 365
 Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly Lys
 370 375 380
 Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro Trp
 385 390 395 400
 Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala Pro
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 Ala Phe Pro Leu Ser Arg Gln Gly Phe Ser Ser Leu Ala Arg Leu Val
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 Ser Asn Ser
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 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro
 20 25 30
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 Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser
 35 40 45

gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa	191
Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu	
50 55 60	
ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc	239
Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro	
65 70 75	
cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc	287
Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser	
80 85 90 95	
acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct	335
Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala	
100 105 110	
gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg	383
Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr	
115 120 125	
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Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu	
130 135 140	
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Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly	
145 150 155	
gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg	527
Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly	
160 165 170 175	
tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa	575
Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu	
180 185 190	
ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca	623
Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro	
195 200 205	
cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc	671
Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu	
210 215 220	
tcc agg agg gga cac cgg gtt cac gag ctg ccc acg tcc tct cca gga	719
Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly	
225 230 235	
ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca	767
Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr	
240 245 250 255	
ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc	815
Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser	
260 265 270	

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Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
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Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg
      290                      295                      300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959
Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala
      305                      310                      315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007
Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala
      320                      325                      330                      335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055
Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg
      340                      345                      350

cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103
Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu
      355                      360                      365

gac ctg ccc cca tgg acc tgg aga cag ggt ttc tcc tca ttg gcc agg 1151
Asp Leu Pro Pro Trp Thr Trp Arg Gln Gly Phe Ser Ser Leu Ala Arg
      370                      375                      380

ctg gtc tcg aac tcc tgacctcaga cgatccacct gcctcagcct cccgaagtgt 1206
Leu Val Ser Asn Ser
      385

tggtgattaca ggcacgagcc actgtgcccc gccatcattc ctttttactg ctgactaata 1266

gtctgctgtg tgaatccacc gctagaaacc cactcatcag ttgatggtca tgtggggtgc 1326

ttctgctatt cgcttattat gaacagtgtt ggaataaacg ttctgtgca ctcttgggca 1386

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<212> PRT
<213> Homo sapiens

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Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala
      35                      40                      45

Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
 50                      55                      60

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 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
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 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 100 105 110
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
 115 120 125
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
 130 135 140
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
 145 150 155 160
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
 165 170 175
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
 180 185 190
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
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Val Ser Asn Ser
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 <212> DNA
 <213> Homo sapiens

<220>
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 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro
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cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct 143
 Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser
 35 40 45

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 Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu
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 Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro
 65 70 75

cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc 287
 Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser
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acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct 335
 Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
 100 105 110

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 Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr
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ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc 431
 Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu
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 Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly
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Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly	
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tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa	575
Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu	
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ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca	623
Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro	
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cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc	671
Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu	
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Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly	
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Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr	
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Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser	
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Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala	
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Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg	
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ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc	959
Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala	
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Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala	
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<213> Homo sapiens
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Val	His	Glu	Leu	Pro	Thr	Ser	Ser	Pro	Gly	Arg	Asp	Pro	Gly	Ser	Thr		
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Asn	Cys	Pro	Arg	Pro	Leu	Gln	Glu	Gly	Thr	Pro	Gly	Ser	Arg	Ala	Ala		
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His	Val	Leu	Ser	Arg	Arg	Gly	His	Arg	Val	His	Glu	Leu	Pro	Thr	Pro		
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Ser	Pro	Gly	Arg	Asp	Pro	Gly	Phe	Met	Ser	Cys	Pro	Arg	Pro	Leu	Gln		
	130					135					140						
Glu	Gly	Thr	Arg	Val	His	Glu	Leu	Pro	Thr	Pro	Ser	Pro	Gly	Gly	Asp		
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				165					170					175			

Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
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 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
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 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270
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 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
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 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
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 <213> Homo sapiens

<220>
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 <222> (3)..(1244)

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Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser	
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Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu	
50 55 60	
ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc	239
Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro	
65 70 75	
cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc	287
Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser	
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Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala	
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Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr	
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Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu	
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Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly	
145 150 155	
gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg	527
Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly	
160 165 170 175	
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Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu	
180 185 190	
ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca	623
Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro	
195 200 205	
cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc	671
Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu	
210 215 220	
tcc agg agg gga cac ccg gtt cac gag ctg ccc acg tcc tct cca gga	719
Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly	
225 230 235	

ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca 767
 Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr
 240 245 250 255

ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser
 260 265 270

acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
 275 280 285

gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg
 290 295 300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala
 305 310 315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala
 320 325 330 335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg
 340 345 350

cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu
 355 360 365

gac ctg ccc cca tgg acc tgg atg cca gtg atg cct gag gtc tgc agg 1151
 Asp Leu Pro Pro Trp Thr Trp Met Pro Val Met Pro Glu Val Cys Arg
 370 375 380

gca gtg cat acg ctc acc gcc tgg ccg ctc agg agc ctg tgc ttg acc 1199
 Ala Val His Thr Leu Thr Ala Trp Pro Leu Arg Ser Leu Cys Leu Thr
 385 390 395

ccc aaa tcc gcc ccc caa ctc cct gtt acc ggc tca ctc ctt cca 1244
 Pro Lys Ser Ala Pro Gln Leu Pro Val Thr Gly Ser Leu Leu Pro
 400 405 410

tgaggggcct tccccagga cagccgatgc tctcctgatg gctcctgccc ttgcagagtg 1304

ctgccccgcg ctgcccacct ggcttgacc ctgcctgag cccctcagg gctctgcgcc 1364

acctcaaccc aggcgtttgt tccgcaggaa cctcccggct cttcccactc gggaaaggaa 1424

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cctgtttgtc actgccccgg ggcttttgca cctgcattcc ctctctctgt gagtgtcctg 1544

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cctgacacac gtaggcattg tgaaatgagt cccacaattg ggctaattaa cacacccatc 1724
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<210> 9

<211> 414

<212> PRT

<213> Homo sapiens

<400> 9

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Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala
35 40 45

Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
50 55 60

Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
65 70 75 80

Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
85 90 95

Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
100 105 110

His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
115 120 125

Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
130 135 140

Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
145 150 155 160

Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
165 170 175

Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
180 185 190

Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
195 200 205

Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
 355 360 365
 Leu Pro Pro Trp Thr Trp Met Pro Val Met Pro Glu Val Cys Arg Ala
 370 375 380
 Val His Thr Leu Thr Ala Trp Pro Leu Arg Ser Leu Cys Leu Thr Pro
 385 390 395 400
 Lys Ser Ala Pro Gln Leu Pro Val Thr Gly Ser Leu Leu Pro
 405 410

<210> 10
 <211> 1744
 <212> DNA
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<220>
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 gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95
 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro
 20 25 30

cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct	143
Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser	
35 40 45	
gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa	191
Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu	
50 55 60	
ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc	239
Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro	
65 70 75	
cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc	287
Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser	
80 85 90 95	
acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct	335
Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala	
100 105 110	
gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg	383
Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr	
115 120 125	
ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc	431
Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu	
130 135 140	
cag gaa ggg acc cgg gtc cac gaa ctg ccc acg ccc tct cca gga ggg	479
Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly	
145 150 155	
gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg	527
Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly	
160 165 170 175	
tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa	575
Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu	
180 185 190	
ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca	623
Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro	
195 200 205	
cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc	671
Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu	
210 215 220	
tcc agg agg gga cac cgg gtt cac gag ctg ccc acg tcc tct cca gga	719
Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly	
225 230 235	
ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca	767
Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr	
240 245 250 255	

ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser
 260 265 270

acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
 275 280 285

gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg
 290 295 300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala
 305 310 315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala
 320 325 330 335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg
 340 345 350

cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu
 355 360 365

gac ctg ccc cca tgg acc tgg gaa cct ccc ggc tct tcc cac tcg gga 1151
 Asp Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly
 370 375 380

aag gaa ggc tct ggg cat gga ggt cgg cca ggc ccc atc ccc gta ccc 1199
 Lys Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro
 385 390 395

tgg ccc ttc ttc ctg ctt cct gtt tgt cac tgc ccc ggg gcc ttt gca 1247
 Trp Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala
 400 405 410 415

cct gca ttc cct ctc tct gtg agt gtc ctg ggg ccc gtt acc cac gtc 1295
 Pro Ala Phe Pro Leu Ser Val Ser Val Leu Gly Pro Val Thr His Val
 420 425 430

acc gtc cca gga tac ctt ttc ttt tct ttc tct ctc tcc agc ttt att 1343
 Thr Val Pro Gly Tyr Leu Phe Phe Ser Phe Ser Leu Ser Ser Phe Ile
 435 440 445

gag gta tagttgacaa ttcaggacgg tgtgcactca aggtatgcag catcacaacc 1399
 Glu Val

tgacacacgt aggcattgtg aaatgagtc cacaattggg ctaattaaca cacccatcac 1459

cttacatggt tacttctttc tgtggtgaga acactaaatt ttaaataagag gacacacagc 1519

ctgggcaaca tagtgagacc ctgtctctac aaatataaaa aaattatctg gacgtggtgg 1579

tgcacacctg tgggtcccagc tacttgggaa gctgaggctg gagaatcact tgagcctggg 1639

aggcggaggt tgcggtgcac tccagcctgg gcgacagagg gaggccctat ctcaaaataa 1699
 ataaataaag gacacattct tatcaaaaaa aaaaaaaaaa aaaaa 1744

<210> 11
 <211> 449
 <212> PRT
 <213> Homo sapiens

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 Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala
 35 40 45
 Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
 50 55 60
 Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
 65 70 75 80
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
 85 90 95
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 100 105 110
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
 115 120 125
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
 130 135 140
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
 145 150 155 160
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
 165 170 175
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
 180 185 190
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240

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<211> 22

<213> Artificial Sequenc.

<220>

<223> Description of Artificial Sequence: Primer

gtagtaacag aatggacttt ga

22

<211> 22

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

agagaggaac agcatcaaag tc

22

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

caaacagggt ccaccgtgga aa

22

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

gtgtttcagc cacatttcca cg

22

<210> 16

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

atccaccgct agaaaccac tc

22

<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

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22

<210> 18

<211> 22

<212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 18
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<210> 19
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 19
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<210> 20
 <211> 18
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 tgtaggacta tattgctc 18

<210> 21
 <211> 18
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 cgacatttag gtgacct 18

<210> 22
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic adapter
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<400> 22
 gtcttcacca cgggg 15

<210> 23
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adapter
oligonucleotide

<400> 23
gtggtgaaga c 11

<210> 24
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 24
gcccttaggg agagcagc 18

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ccacatcgtg cctttgtgta 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
cactgtgtta aaacgcctgg 20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gttgggatta caggcacgag 20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
cagaagcaac ccacatgacc 20

<210> 29
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 29
actacaggtt tgcaccacca 20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
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<210> 31
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
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<210> 32
<211> 20
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<220>

<223> Description of Artificial Sequence: Primer

<400> 32

actcgggaaa ggaaggctct

20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 33

cataccttga gtgcacaccg

20

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

gacagtctgc tccacatcca

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<210> 35

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

tggagatgaa gtcttgctct tg

22

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

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<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

cccaggctgt gtgtcctcta

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<210> 38

<211> 1124

<212> DNA

<213> Homo sapiens

<400> 38

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tccacgagct ggccacgtcc tctgcaggaa gggacccggg gtccacgagc tgccacgtc 180
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<210> 39

<211> 289

<212> DNA

<213> Homo sapiens

<400> 39

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tcctttttac tgctgactaa tagtctgctg tgtgaatcca ccgctagaaa cccactcatc 180
agttgatggg catgtgggtt gcttctgcta ttcgcttatt atgaacagtg ctggaataaa 240
cgttcctgtg cactcttggg catacgccca ggagtggaaac tgctgggtc 289

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<210> 40

<211> 139

<212> DNA

<213> Homo sapiens

<400> 40

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gaacctcccc gctcttccca ctccgggaaag gaaggctctg ggcattggagg tcggccaggc 60
cccatccccg taccctggcc cttcttccct cttctctgtt gtcactgccc cggggccttt 120

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gcacctgcat tccctctct

139

<210> 41

<211> 49

<212> DNA

<213> Homo sapiens

<400> 41

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49

<210> 42

<211> 866

<212> DNA

<213> Homo sapiens

<400> 42

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cctgacacac gtaggcattg tgaaatgagt cccacaattg ggctaattaa cacacccatc 600
accttacatg gttacttctt tctgtggtga gaacactaaa ttttaaatag aggacacaca 660
gcctgggcaa catagtgaga ccctgtctct acaaatataa aaaaattatc tggacgtggt 720
ggtgcacacc tgtggtccca gctacttggg aagctgaggc tggagaatca cttgagcctg 780
ggaggcggag gttgcggtgc actccagcct gggcgacaga gggaggccct atctcaaaat 840
aaataaataa aggacacatt cttatc 866

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<210> 43

<211> 387

<212> DNA

<213> Homo sapiens

<400> 43

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ctttattgag gtatagttga caattcagga cggtgtgcac tcaaggtatg cagcatcaca 60
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caccttacat ggttacttct ttctgtggtg agaacactaa attttaataa gaggacacac 180
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tggtgcacac ctgtggtccc agctacttgg gaagctgagg ctggagaatc acttgagcct 300
gggaggcgga ggttgcggtg cactccagcc tgggcgacag agggaggccc tatctcaaaa 360
taaataaata aaggacacat tcttatc 387

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<210> 44

<211> 599

<212> DNA

<213> Homo sapiens

<400> 44

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gaacctccccg gctcttccca ctccgggaaag gaaggctctg ggcattggagg tcggccaggc 60
cccatccccg taccctggcc cttcttctct cttctgttt gtcaactgcc cggggccttt 120

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gcacctgcat tccctctctc tgtgagtgtc ctggggcccg ttacccacgt caccgtccca 180
ggataccttt tcttttcttt ctctctctcc agctttattg aggtatagtt gacaattcag 240
gacggtgtgc actcaaggta tgcagcatca caacctgaca cacgtaggca ttgtgaaatg 300
agtcccacaa ttgggctaata taacacaccc atcaccttac atgggtactt ctttctgtgg 360
tgagaacact aaatttttaa tagaggacac acagcctggg caacatagtg agaccctgtc 420
tctacaaata taaaaaaatt atctggacgt ggtggtgcac acctgtggtc ccagctactt 480
gggaagctga ggctggagaa tcacttgagc ctgggagggc gaggttgagg tgcactccag 540
cctgggagac agagggaggc cctatctcaa aataaataaa taaaggacac attcttacc 599

```

```

<210> 45
<211> 1028
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> modified_base
<222> (267)
<223> a, t, c or g

```

```

<400> 45
cgggcggtga tatctcttca tagagagcgc tcagacagcg tgcgttaatc tgcgtcgata 60
tatagagatc tttatcactg agtagataga acgtacatga atgtacgaac agtccagacg 120
agtaacttga ctaggataag atagacagta ccaactaatg agacaagaag agggaaatcat 180
atagaatcat gtagtctgag tctagcgagt gtcgacatga tcacaagcga aatacagact 240
atgagaagag gtagaaataa taagtanact gagaagagag gtcatatgta catacaaatac 300
agtaaagcaa tagaaattga atacattata agccacagtt acagaattag cctaatttaa 360
caaccatggc aagcgagtta tatcaaacat agaagagtaa actctatcga ccatgggtag 420
gaacgaataa aggcgtcgag aagacaataa gaatgctgtg taaacagcaa tacaagagaa 480
tagcaccact gaagcagacc aaaggcgtca ccggggaagt aggggaaggg cacctcacia 540
ggagaggaaa gggcagtcct gatcttgaaa atttcagtga aaagacagtg ttgttcccgg 600
aggcagctta gtgatcccg atcgactctg aagaggaccc tgagggtagg ggatttttgg 660
gcctgaccgg cctatgctga acgcccaccg ggaattcagg gagaaacacg gggccccggc 720
ttccaggaga gcagccaggc cacagccctg aggacgggca aaccccaccc aggcacgggtg 780
agagggaggc cgcccaggcc tggggcctgg cggcagggga tgaagtggac cagagccccg 840
caaatcctaa cgtgggtgag cagtgaacct gtgtggctgc gagtggctcc gttttggggc 900
tgtttgttcc tgcagcaaat gatgccagcc ctgacggaac cagtgcacgt ccaccacgag 960
ctgcccacgt cctctccagg aagggacccg ggtccacgag ctgcccacgt cctctccagg 1020
aagggacc 1028

```

```

<210> 46
<211> 40
<212> DNA
<213> Homo sapiens

```

```

<400> 46
actacaggtt tgcaccacca tgtcctgcta attttttttt 40

```

```

<210> 47
<211> 40
<212> DNA
<213> Homo sapiens

```

```

<400> 47
actacaggtt tgcaccacgg tgtcctgcta attttttttt 40

```

<210> 48
<211> 39
<212> DNA
<213> Homo sapiens

<400> 48
tgtgcactct tgggcatacg cctaggagtg gaactgctg 39

<210> 49
<211> 39
<212> DNA
<213> Homo sapiens

<400> 49
tgtgcactct tgggcatatg cctaggagtg gaactgctg 39

<210> 50
<211> 39
<212> DNA
<213> Homo sapiens

<400> 50
gggctctgcg ccacctcaac ccaggcggtt gttccgcag 39

<210> 51
<211> 39
<212> DNA
<213> Homo sapiens

<400> 51
gggctctgcg ccacctcaac tcaggcggtt gttccgcag 39